>AF249738 ACCESSION:AF249738 NID: gi 8571425 gb AF249738.1 AF249738 Mus musculus Pb99 gene sequence Length = 2127

Score = 358 bits (910), Expect(3) = 0.0
Identities = 210/293 (72%), Positives = 233/293 (80%)
Frame = +1

Query: 206 RPPPNMTLTCVFWDVTKGTTGDWSSEGCSTEVRPEGTVCCCDHLTFFALLLRPTLDQSTV 265 R P N+ LTCVFWD+ KG DW S CST TVC CDHLTFFALLLRP LD +T

Sbjct: 748 RSPHNVILTCVFWDMAKG---DWDSH-CSTVPGDGRTVCRCDHLTFFALLLRPILDLATA 915

Query: 266 HILTRISQAGGGVSMIFLAFTIILYAFLRLSRERFKSEDAPKIHVALGGSLFLLNLAFLV 325 LTRISQAG VSMIFLAFT++LY R S +RFKSEDAPKIH+AL SLFLLNL FL

Sbjct: 916 QTLTRISQAGSAVSMIFLAFTMVLYVAFRFSLQRFKSEDAPKIHMALSISLFLLNLTFLI 1095

Query: 326 NVGSGSKGSDAACWARGAVFHYFLLCAFTWMGLEAFHLYLLAVRVFNTYFGHYFLKLSLV 385

NVGS S+G A+CW R A+FHYFLLC FTWMGLEAFHLYLLA+RVFNTYFGHYFLKLSL+
Sbjct: 1096 NVGSSSQGPPASCWVRAAIFHYFLLCVFTWMGLEAFHLYLLAIRVFNTYFGHYFLKLSLL 1275

Ouery: 386 GWGLPALMVIGTGSANSYGLYTIRDRENRTSLELCWFREGTTMYALYITVHGYFLITFLF 445

WGLP L+VIG GS+NSYG+YTIRD+ENRTSLELCWF++ ALY TVHGYFL+TFLF
Sbjct: 1276 AWGLPVLVVIGAGSSNSYGVYTIRDOENRTSLELCWFQKEP---ALYATVHGYFLVTFLF 1446

Query: 446 GMVVLALVVWKIFTLSRATAVKERGKNRKKVLTLLGLSSLVGVTWGLAIFTPL 498 G VVLALV WKIFTL TA K +G K VLT+LGLSSLVG+TWGLA+ TPL

Sbjct: 1447 GAVVLALVAWKIFTLPSVTAGKGQGPTWKSVLTVLGLSSLVGMTWGLAVLTPL 1605

Score = 245 bits (618), Expect(3) = 0.0 Identities = 129/215 (60%), Positives = 159/215 (74%), Gaps = 2/215 (0%) Frame = +2

Query: 1 MATPRGLGALLLLLLPTSGQEKPTEGPRNTC--LGSNNMYDIFNLNDKALCFTKCRQSG 58
MAT R LG L LLL + E+ TE PRN C L + YD F+LND A CFTKC QS

Sbjct: 17 MATARSLGLLFFLLL---TSDEETTEEPRNVCRRLQEGHEYDTFDLNDTAQCFTKCGQSE 187

Query: 59 SDSCNVENLQRYWLNYEAHLMKEGLTQKVNTPFLKALVQNLSTNTAEDFYFSLEPSQVPR 118 C+V NLQRYWLNYE++L++ + + + V+ PF+KAL+QN+ST+ +ED +SL SQ+PR

Sbjct: 188 HSPCDVGNLORYWLNYESYLLENSM-ETVDMPFVKALIONISTDVSEDLLYSLMLSOIPR 364

Query: 119 QVMKDEDKPPDRVRLPKSLFRSLPGNRSVVRLAVTILDIGPGTLFKGPRLGLGGDGSGVLN 178

QVM+ ED+P D VRLPKSLF +LPGNRS VRLA+T+LDIG G +FKGP+L GS VLN

Sbjct: 365 OVMOGEDEPADGVRLPKSLFGALPGNRSAVRLAITVLDIGAGNVFKGPKLLEDKGSSVLN 544

Query: 179 NRLVGLSVGQMHVTKLAEPLEIVFSHQRPPPNMTL 213 NR+VGLSVGQMH T L+EP+EI FSH+R PP M L

Sbjct: 545 NRMVGLSVGQMHATGLSEPVEITFSHERQPPAMIL 649

```
Score = 84.7 bits (206), Expect(3) = 0.0 Identities = 41/54 (75%), Positives = 45/54 (82%), Gaps = 1/54 (1%) Frame = +3
```

Query: 497 PLGLSTVY1FALFNSLQGVF1CCMFTLIVLPSQGTTVSSS-TARLDQAHSASQE 549 P GLST+Y+F L NSLQG+F1 CWF ILY P+QSTT SSS TARLDQAHS SQE Sbjct: 1599 PPGLST1VYFTLLNSLQGLF1FCWF1LLYFPTQSTTASSSGTARLDQAHSVSQE 1760